

PATENT
671308-2001.1**AMENDMENTS TO THE SPECIFICATION**

Please amend the specification without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows.

On page 1, line 5, please insert the following paragraph between the title and the background of the invention:

This application is a continuation application of U.S. patent application Serial No. 09/816,319 filed March 26, 2001, now abandoned, which claims priority to Japanese patent application Serial No. 2000-287688 filed September 21, 2000.

Please replace the paragraph on page 22, line 14 to page 23, line 1, with the following paragraph:

The homology of a nucleotide sequence or an amino acid sequence can be determined using the algorithm "BLAST" by Karlin and Altschil (Proc. Natl. Acad. Sci. USA, 90, 5873-5877 (1993)). The programs called "BLASTN" and "BLASTX" have developed based on the above algorithm (J. Mol. Biol., 215, 403-410 (1990)). In the case of analyzing a nucleotide sequence based on BLAST, the parameter can be set to e.g. score=100, wordlength=12. And in the case of analyzing an amino acid sequence based on BLASTX, the parameter can be set to e.g. score=50, wordlength=3. In the case of using BLAST or Gapped BLAST program, a default parameter of each program can be used. The specific analysis method of using the above programs are known in the art (<http://www.ncbi.nlm.nih.gov>).